



IFWO

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION:** US/10/600,158

**DATE:** 08/04/2004  
**TIME:** 11:03:09

**Input Set :** N:\CrF3\RULE60\10600158.raw  
**Output Set:** N:\CRF4\08042004\J600158.raw

1 <110> APPLICANT: Wang, Xin Wei  
 2 Harris, Curtis C.  
 3 Fornace Jr., Albert J.  
 4 Coursen, Jill D.  
 5 Zhan, Qimin  
 6 The Government of the United States of America  
 7 as represented by the Secretary of the  
 8 Department of Health and Human Services  
 9 <120> TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45  
 10 Polypeptide Activity, and Inhibitors of Such Activity  
 11 <130> FILE REFERENCE: 015280-367100US  
 12 <140> CURRENT APPLICATION NUMBER: US/10/600,158  
 13 <141> CURRENT FILING DATE: 2003-06-20  
 14 <150> PRIOR APPLICATION NUMBER: US/09/534,811  
 15 <151> PRIOR FILING DATE: 2000-03-24  
 16 <150> PRIOR APPLICATION NUMBER: US 60/126,069  
 17 <151> PRIOR FILING DATE: 1999-03-25  
 18 <160> NUMBER OF SEQ ID NOS: 32  
 19 <170> SOFTWARE: PatentIn Ver. 2.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 1343  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Homo sapiens  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: CDS  
 27 <222> LOCATION: (284)..(781)  
 28 <223> OTHER INFORMATION: human growth arrest and DNA-damage-inducible  
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 30 <400> SEQUENCE: 1  
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 32 cggggagcga gcgagcaagc aaggcgggag gggtgcccg agctgcggcg gctggcacag 120  
 33 gagggaggac ccgggcgggc gaggggcggc cgagagagcgc cagggcctga gctgccggag 180  
 34 cggcgccctgt gagtgagtgc agaaaaggcagg cgcccgccgc ctggccgtgg caggagcagc 240  
 35 ccgcacgccc cgctctctcc ctgggcgacc tgcagttgc aat atg act ttg gag 295  
 36 Met Thr Leu Glu  
 37 1  
 38 gaa ttc tcg gct gga gag cag aag acc gaa agg atg gat aag gtg ggg 343  
 39 Glu Phe Ser Ala Gly Glu Gln Lys Thr Glu Arg Met Asp Lys Val Gly  
 40 5 10 15 20  
 41 gat gcc ctg gag gaa gtg ctc agc aaa gcc ctg agt cag cgc acg atc 391  
 42 Asp Ala Leu Glu Glu Val Leu Ser Lys Ala Leu Ser Gln Arg Thr Ile  
 43 25 30 35  
 44 act gtc ggg gtg tac gaa gcg gcc aag ctg ctc aac gtc gac ccc gat 439

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45 Thr Val Gly Val Tyr Glu Ala Ala Lys Leu Leu Asn Val Asp Pro Asp  
 46 40 45 50  
 47 aac gtg gtg ttg tgc ctg ctg gcg gac gag gac gac aga gat 487  
 48 Asn Val Val Leu Cys Leu Leu Ala Ala Asp Glu Asp Asp Arg Asp  
 49 55 60 65  
 50 gtg gct ctg cag atc cac ttc acc ctg atc cag gcg ttt tgc tgc gag 535  
 51 Val Ala Leu Gln Ile His Phe Thr Leu Ile Gln Ala Phe Cys Cys Glu  
 52 70 75 80  
 53 aac gac atc aac atc ctg cgc gtc agc aac ccg ggc cg 583  
 54 Asn Asp Ile Asn Ile Leu Arg Val Ser Asn Pro Gly Arg Leu Ala Glu  
 55 85 90 95 100  
 56 ctc ctg ctc ttg gag acc gac gct ggc ccc gcg gac gag ggc gcc 631  
 57 Leu Leu Leu Leu Glu Thr Asp Ala Gly Pro Ala Ala Ser Glu Gly Ala  
 58 105 110 115  
 59 gag cag ccc ccg gac ctg cac tgc gtg ctg gtg acg aat cca cat tca 679  
 60 Glu Gln Pro Pro Asp Leu His Cys Val Leu Val Thr Asn Pro His Ser  
 61 120 125 130  
 62 tct caa tgg aag gat cct gcc tta agt caa ctt att tgt ttt tgc cgg 727  
 63 Ser Gln Trp Lys Asp Pro Ala Leu Ser Gln Leu Ile Cys Phe Cys Arg  
 64 135 140 145  
 65 gaa agt cgc tac atg gat caa tgg gtt cca gtg att aat ctc cct gaa 775  
 66 Glu Ser Arg Tyr Met Asp Gln Trp Val Pro Val Ile Asn Leu Pro Glu  
 67 150 155 160  
 68 cgg tga tggcatctga atgaaaataa ctgaaccaa ttgcactgaa gttttgaaa 831  
 69 Arg  
 70 165  
 71 taccttgta gttactcaag cagttactcc ctacactgat gcaaggatta cagaaaactga 891  
 72 tgccaaagggtt ctgagttagt tcaactacat gttctggggg cccggagata gatgactttg 951  
 73 cagatggaaa gaggtgaaaa tgaagaagga agctgtttg aaacagaaaa ataagtcaaa 1011  
 74 aggaacaaaa attacaaaga accatgcagg aaggaaaaact atgtattaat tttagaatgg 1071  
 75 tgagttacat taaaataaac caaatatgtt aaagtttaag tggcagcca tagtttggt 1131  
 76 atttttgggtt tatatgccct caagtaaaag aaaagccgaa agggttaatc atatttgaaa 1191  
 77 accatatttt attgtatttt gatgagat taaattctca aagttttatt ataaattctca 1251  
 78 ctaagttatt ttatgacatg aaaagttatt tatgctataa atttttgaa acacaatacc 1311  
 79 tacaataaac tggtatgaat aattgcatca tt 1343  
 81 <210> SEQ ID NO: 2  
 82 <211> LENGTH: 165  
 83 <212> TYPE: PRT  
 84 <213> ORGANISM: Homo sapiens  
 85 <400> SEQUENCE: 2  
 86 Met Thr Leu Glu Glu Phe Ser Ala Gly Glu Gln Lys Thr Glu Arg Met  
 87 1 5 10 15  
 88 Asp Lys Val Gly Asp Ala Leu Glu Glu Val Leu Ser Lys Ala Leu Ser  
 89 20 25 30  
 90 Gln Arg Thr Ile Thr Val Gly Val Tyr Glu Ala Ala Lys Leu Leu Asn  
 91 35 40 45  
 92 Val Asp Pro Asp Asn Val Val Leu Cys Leu Leu Ala Ala Asp Glu Asp  
 93 50 55 60  
 94 Asp Asp Arg Asp Val Ala Leu Gln Ile His Phe Thr Leu Ile Gln Ala

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95      65          70          75          80
96 Phe Cys Cys Glu Asn Asp Ile Asn Ile Leu Arg Val Ser Asn Pro Gly
97           85          90          95
98 Arg Leu Ala Glu Leu Leu Leu Glu Thr Asp Ala Gly Pro Ala Ala
99           100         105         110
100 Ser Glu Gly Ala Glu Gln Pro Pro Asp Leu His Cys Val Leu Val Thr
101           115         120         125
102 Asn Pro His Ser Ser Gln Trp Lys Asp Pro Ala Leu Ser Gln Leu Ile
103           130         135         140
104 Cys Phe Cys Arg Glu Ser Arg Tyr Met Asp Gln Trp Val Pro Val Ile
105           145         150         155         160
106 Asn Leu Pro Glu Arg
107           165
109 <210> SEQ ID NO: 3
110 <211> LENGTH: 31
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112 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR
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116 <400> SEQUENCE: 3
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120 <212> TYPE: DNA
121 <213> ORGANISM: Artificial Sequence
122 <220> FEATURE:
123 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR
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125 <400> SEQUENCE: 4
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129 <212> TYPE: PRT
130 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:
132 <223> OTHER INFORMATION: Description of Artificial Sequence:GADD45
133   subsequence acidic motif amino acid residues
134   62-67; exemplary peptide inhibiting GADD45-related
135   dissociation of Cdc2/cyclin B1 complexes
136 <400> SEQUENCE: 5
137   Asp Glu Asp Asp Asp Arg
138     1          5
139 <210> SEQ ID NO: 6
140 <211> LENGTH: 160
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
143 <220> FEATURE:
144 <223> OTHER INFORMATION: human growth arrest and DNA-damage-inducible

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148      protein (hGADD45beta)
149 <400> SEQUENCE: 6
150      Met Thr Leu Glu Glu Leu Val Ala Cys Asp Asn Ala Ala Gln Lys Met
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152      Gln Thr Val Thr Ala Ala Val Glu Glu Leu Leu Val Ala Ala Gln Arg
153          20          25           30
154      Gln Asp Arg Leu Thr Val Gly Val Tyr Glu Ser Ala Lys Leu Met Asn
155          35          40           45
156      Val Asp Pro Asp Ser Val Val Leu Cys Leu Leu Ala Ile Asp Glu Glu
157          50          55           60
158      Glu Glu Asp Asp Ile Ala Leu Gln Ile His Phe Thr Leu Ile Gln Ser
159          65          70           75           80
160      Phe Cys Cys Asp Asn Asp Ile Asn Ile Val Arg Val Ser Gly Met Gln
161          85          90           95
162      Arg Leu Ala Gln Leu Leu Gly Glu Pro Ala Glu Thr Gln Gly Thr Thr
163          100         105           110
164      Glu Ala Arg Asp Leu His Cys Leu Leu Val Thr Asn Pro His Thr Asp
165          115         120           125
166      Ala Trp Lys Ser His Gly Leu Val Glu Val Ala Ser Tyr Cys Glu Glu
167          130         135           140
168      Ser Arg Gly Asn Asn Gln Trp Val Pro Tyr Ile Ser Leu Gln Glu Arg
169          145         150           155           160
171 <210> SEQ ID NO: 7
172 <211> LENGTH: 159
173 <212> TYPE: PRT
174 <213> ORGANISM: Homo sapiens
175 <220> FEATURE:
176 <223> OTHER INFORMATION: human growth arrest and DNA-damage-inducible
177     protein (hGADD45gamma)
178 <400> SEQUENCE: 7
179      Met Thr Leu Glu Glu Val Arg Gly Gln Asp Thr Val Pro Glu Ser Thr
180          1           5           10           15
181      Ala Arg Met Gln Gly Ala Gly Lys Ala Leu His Glu Leu Leu Ser
182          20          25           30
183      Ala Gln Arg Gln Gly Cys Leu Thr Ala Gly Val Tyr Glu Ser Ala Lys
184          35          40           45
185      Val Leu Asn Val Asp Pro Asp Asn Val Thr Phe Cys Val Leu Ala Ala
186          50          55           60
187      Gly Glu Glu Asp Glu Gly Asp Ile Ala Leu Gln Ile His Phe Thr Leu
188          65          70           75           80
189      Ile Gln Ala Phe Cys Cys Glu Asn Asp Ile Asp Ile Val Arg Val Gly
190          85          90           95
191      Asp Val Gln Arg Leu Ala Ala Ile Val Gly Ala Gly Glu Ala Gly
192          100         105           110
193      Ala Pro Gly Asp Leu His Cys Ile Leu Ile Ser Asn Pro Asn Glu Asp
194          115         120           125
195      Ala Trp Lys Asp Pro Ala Leu Glu Lys Leu Ser Leu Phe Cys Glu Glu
196          130         135           140
197      Ser Arg Ser Val Asn Asp Trp Val Pro Ser Ile Thr Leu Pro Glu

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204 <220> FEATURE:
205 <223> OTHER INFORMATION: mouse growth arrest and DNA-damage-inducible
206 protein (mGADD45)
207 <400> SEQUENCE: 8
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209     1           5           10           15
210 Asp Thr Val Gly Asp Ala Leu Glu Glu Val Leu Ser Lys Ala Arg Ser
211     20          25          30
212 Gln Arg Thr Ile Thr Val Gly Val Tyr Glu Ala Ala Lys Leu Leu Asn
213     35          40          45
214 Val Asp Pro Asp Asn Val Val Leu Cys Leu Leu Ala Ala Asp Glu Asp
215     50          55          60
216 Asp Asp Arg Asp Val Ala Leu Gln Ile His Phe Thr Leu Ile Arg Ala
217     65          70          75          80
218 Phe Cys Cys Glu Asn Asp Ile Asn Ile Leu Arg Val Ser Asn Pro Gly
219     85          90          95
220 Arg Leu Ala Glu Leu Leu Leu Glu Asn Asp Ala Gly Pro Ala Glu
221     100         105         110
222 Ser Gly Gly Ala Ala Gln Thr Pro Asp Leu His Cys Val Leu Val Thr
223     115         120         125
224 Asn Pro His Ser Ser Gln Trp Lys Asp Pro Ala Leu Ser Gln Leu Ile
225     130         135         140
226 Cys Phe Cys Arg Glu Ser Arg Tyr Met Asp Gln Trp Val Pro Val Ile
227     145         150         155         160
228 Asn Leu Pro Glu Arg
229     165
230
231 <210> SEQ ID NO: 9
232 <211> LENGTH: 165
233 <212> TYPE: PRT
234 <213> ORGANISM: Rattus norvegicus
235 <220> FEATURE:
236 <223> OTHER INFORMATION: rat growth arrest and DNA-damage-inducible protein
237 (rGADD45)
238 <400> SEQUENCE: 9
239 Met Thr Leu Glu Glu Phe Ser Ala Ala Glu Gln Lys Ile Glu Arg Met
240     1           5           10           15
241 Asp Thr Val Gly Asp Ala Leu Glu Glu Val Leu Ser Lys Ala Arg Ser
242     20          25          30
243 Gln Arg Thr Ile Thr Val Gly Val Tyr Glu Ala Ala Lys Leu Leu Asn
244     35          40          45
245 Val Asp Pro Asp Asn Val Val Leu Cys Leu Leu Ala Ala Asp Glu Asp
246     50          55          60
247 Asp Asp Arg Asp Val Ala Leu Gln Ile His Phe Thr Leu Ile Arg Ala
248     65          70          75          80
  
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**VERIFICATION SUMMARY**

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Output Set: N:\CRF4\08042004\J600158.raw